

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/560,237  
Source: IFWP  
Date Processed by STIC: 4/27/07

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 04/27/2007

PATENT APPLICATION: US/10/560,237

TIME: 11:45:32

Input Set : A:\05081151.APP

Output Set: N:\CRF4\04272007\J560237.raw

3 <110> APPLICANT: DUCOMMUN, BERNARD  
 4 MONSARRAT, BERNARD  
 5 PRIGENT, CLAUDE  
 7 <120> TITLE OF INVENTION: NOVEL PHOSPHORYLATED SEQUENCES OF CDC25B  
 PHOSPHATASE,  
 8 ANTIBODIES DIRECTED AGAINST THESE SEQUENCES AS WELL AS  
 9 THEIR USE  
 11 <130> FILE REFERENCE: 0508-1151  
 13 <140> CURRENT APPLICATION NUMBER: 10/560,237  
 14 <141> CURRENT FILING DATE: 2005-12-12  
 16 <150> PRIOR APPLICATION NUMBER: PCT/FR04/001416  
 17 <151> PRIOR FILING DATE: 2004-06-08  
 19 <150> PRIOR APPLICATION NUMBER: FR 0307095  
 20 <151> PRIOR FILING DATE: 2003-06-12  
 22 <160> NUMBER OF SEQ ID NOS: 11  
 24 <170> SOFTWARE: PatentIn Ver. 3.3  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 19  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Homo sapiens  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: MOD\_RES  
 33 <222> LOCATION: (10)  
 34 <223> OTHER INFORMATION: PHOSPHORYLATION  
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 38 1 5 10 15  
 40 Gln Gln Glu  
 44 <210> SEQ ID NO: 2  
 45 <211> LENGTH: 14  
 46 <212> TYPE: PRT  
 47 <213> ORGANISM: Homo sapiens  
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 51 <222> LOCATION: (7)  
 52 <223> OTHER INFORMATION: PHOSPHORYLATION  
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 56 1 5 10  
 59 <210> SEQ ID NO: 3  
 60 <211> LENGTH: 566  
 61 <212> TYPE: PRT  
 62 <213> ORGANISM: Homo sapiens  
 64 <220> FEATURE:

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66 <222> LOCATION: (339)
67 <223> OTHER INFORMATION: PHOSPHORYLATION
69 <400> SEQUENCE: 3
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73 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
74           20           25           30
76 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
77           35           40           45
79 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
80           50           55           60
82 Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala
83   65           70           75           80
85 Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly
86           85           90           95
88 Leu Cys Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln
89           100          105          110
91 Thr Phe Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu
92           115          120          125
94 Gln Phe Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly
95           130          135          140
97 His Ser Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly
98 145          150          155          160
100 Arg Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu
101           165          170          175
103 Asp Lys Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr
104           180          185          190
106 His Pro Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu
107           195          200          205
109 Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser
110          210          215          220
112 Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly
113 225          230          235          240
115 Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly
116           245          250          255
118 Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp Asp Asp Ala Val Pro
119           260          265          270
121 Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu Val Lys Thr Leu Glu
122           275          280          285
124 Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser Lys Cys Gln Arg Leu
125           290          295          300
127 Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile Arg Pro Ile Leu Lys
128 305          310          315          320
130 Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg
131           325          330          335
133 Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln Glu Ala Glu Glu Pro
134           340          345          350
136 Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys His Asp Glu Ile Glu

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137          355          360          365
139 Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile Gly Asp Tyr Ser Lys
140          370          375          380
142 Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp Leu Lys Tyr
143 385          390          395          400
145 Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys Phe Ser Asn
146          405          410          415
148 Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro Tyr Glu Tyr
149          420          425          430
151 Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu Glu Arg Asp
152          435          440          445
154 Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys Ser Leu Asp
155          450          455          460
157 Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser Glu Arg Gly
158 465          470          475          480
160 Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala Val Asn Asp
161          485          490          495
163 Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys Gly Gly Tyr
164          500          505          510
166 Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro Gln Asp Tyr
167          515          520          525
169 Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys Thr Phe Arg
170          530          535          540
172 Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg Glu Leu Cys
173 545          550          555          560
175 Ser Arg Leu Gln Asp Gln
176          565
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 539
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <220> FEATURE:
185 <221> NAME/KEY: MOD_RES
186 <222> LOCATION: (312)
187 <223> OTHER INFORMATION: PHOSPHORYLATION
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191 1          5          10          15
193 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
194          20          25          30
196 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
197          35          40          45
199 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
200          50          55          60
202 Leu Gly Ser Glu Thr Pro Lys Ser Gln Val Gly Thr Leu Leu Phe Arg
203 65          70          75          80
205 Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala Ser Glu
206          85          90          95
208 Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly Leu Cys

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209          100          105          110
211 Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln Thr Phe
212          115          120          125
214 Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu Gln Phe
215          130          135          140
217 Ala Ile Arg Arg Phe Gln Ser Met Pro Asp Gly Phe Val Phe Lys Met
218 145          150          155          160
220 Pro Trp Lys Pro Thr His Pro Ser Ser Thr His Ala Leu Ala Glu Trp
221          165          170          175
223 Ala Ser Arg Arg Glu Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp
224          180          185          190
226 Leu Met Cys Leu Ser Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser
227          195          200          205
229 Pro Leu Ala Leu Gly Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr
230          210          215          220
232 Glu Glu Asp Asp Gly Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp
233 225          230          235          240
235 Asp Asp Ala Val Pro Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu
236          245          250          255
238 Val Lys Thr Leu Glu Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser
239          260          265          270
241 Lys Cys Gln Arg Leu Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile
242          275          280          285
244 Arg Pro Ile Leu Lys Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro
245          290          295          300
247 Val Gln Asn Lys Arg Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln
248 305          310          315          320
250 Glu Ala Glu Glu Pro Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys
251          325          330          335
253 His Asp Glu Ile Glu Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile
254          340          345          350
256 Gly Asp Tyr Ser Lys Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His
257          355          360          365
259 Gln Asp Leu Lys Tyr Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr
260          370          375          380
262 Gly Lys Phe Ser Asn Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg
263 385          390          395          400
265 Tyr Pro Tyr Glu Tyr Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu
266          405          410          415
268 Pro Leu Glu Arg Asp Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala
269          420          425          430
271 Pro Cys Ser Leu Asp Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe
272          435          440          445
274 Ser Ser Glu Arg Gly Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp
275          450          455          460
277 Arg Ala Val Asn Asp Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile
278 465          470          475          480
280 Leu Lys Gly Gly Tyr Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys
281          485          490          495

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283 Glu Pro Gln Asp Tyr Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu
284           500           505           510
286 Leu Lys Thr Phe Arg Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser
287           515           520           525
289 Arg Arg Glu Leu Cys Ser Arg Leu Gln Asp Gln
290           530           535
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 580
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <220> FEATURE:
299 <221> NAME/KEY: MOD_RES
300 <222> LOCATION: (353)
301 <223> OTHER INFORMATION: PHOSPHORYLATION
303 <400> SEQUENCE: 5
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305   1           5           10           15
307 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
308           20           25           30
310 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
311           35           40           45
313 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
314           50           55           60
316 Leu Gly Ser Glu Thr Pro Lys Ser Gln Val Gly Thr Leu Leu Phe Arg
317   65           70           75           80
319 Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala Ser Glu
320           85           90           95
322 Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly Leu Cys
323           100          105          110
325 Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln Thr Phe
326           115          120          125
328 Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu Gln Phe
329           130          135          140
331 Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly His Ser
332 145           150           155           160
334 Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly Arg Arg
335           165          170          175
337 Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu Asp Lys
338           180          185          190
340 Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr His Pro
341           195          200          205
343 Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu Ala Phe
344           210          215          220
346 Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser Pro Asp
347 225           230           235           240
349 Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly Arg Phe
350           245          250          255
352 Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly Phe Val
353           260          265          270

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**VERIFICATION SUMMARY**

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